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in search, using sw model

ril 2, 2004, 10:11:59 ; Search time 54 Seconds
 (without alignments)
 612.186 Million cell updates/sec

-10-066-273-9

OSUM62

pop 10.0 , Gapext: 0.5

86107 seqs, 282547505 residues

ts satisfying chosen parameters:

9th: 0
 9th: 2000000000

minimum Match 0%
 maximum Match 100%
 listing first 45 summaries

- Geneseq_29Jan04: *
 - geneseqP1980s: *
 - geneseqP1990s: *
 - geneseqP000s: *
 - GeneseqP2001s: *
 - geneseqP2002s: *
 - GeneseqP2003as: *
 - geneseqP2003bs: *
 - geneseqP2004s: *

the number of results predicted by chance to have a
 r than or equal to the score of the result being printed,
 ed by analysis of the total score distribution.

RESULTS

1
 AAB31180 standard; protein; 117 AA.
 XX
 AAB31180;
 AC
 XX
 DT 20-APR-2001 (first entry)
 XX

DDE Amino acid sequence of human polypeptide PRO444.
 XX Human; secreted protein; transmembrane protein; PRO196; PRO444; F
 KW PRO185; PRO210; PRO215; PRO217; PRO212; PRO288; PRO1361;
 KW PRO1183; PRO1272; PRO1419; PRO4999; PRO1710; PRO248; PRO353; PRO1
 KW PRO1600; PRO940; PRO533; PRO301; PRO187; PRO37; PRO1411; PRO3
 KW PRO246; PRO255; PRO6003; PRO6004; PRO350; PRO26
 KW PRO6309; cell death; genetic disorder; transgenic animal; gene tr
 XX Homo sapiens.
 OS

KEY

Peptide
 PT Key
 PT Peptide
 PT Location/Qualifiers
 1. .16 "Signal peptide"
 1B. .24
 /note= "N-myristoylation site"
 /note= "N-myristoylation site"
 32. .38
 /note= "N-myristoylation site"
 /note= "N-myristoylation site"
 34. .40
 /note= "N-myristoylation site"
 /note= "N-myristoylation site"
 35. .41
 /note= "N-myristoylation site"
 /note= "N-myristoylation site"
 51. .57
 /note= "N-myristoylation site"

SUMMARIES

Query	Length	DB	ID	Description
-	-	-	-	-
0.0	117	4	AAB31180	Aab31180 Amino aci
0.0	117	6	ABO25151	Abo25151 Novel hum
0.0	117	6	ABU67269	Abu67269 Novel hum
0.0	117	6	ABU7037	Abu72037 Novel hum
0.0	117	6	ABU67138	Abu67138 Novel hum
0.0	117	6	ABU79780	Abu79780 Human sec
0.0	117	6	ABO33583	Abo33583 Novel hum
0.0	117	6	ADA47181	Ada47181 Human sec
0.0	117	7	ABO44436	Abo44436 Human sec
0.0	117	7	ABO33460	Abo33460 Novel hum
0.0	117	7	ABO19838	Abo19838 Human sec
0.0	117	7	ADC19875	Adc19875 Human PRO
0.0	117	7	ADD10295	Add10295 Human sec
0.0	117	7	ADD11255	Add11255 Human sec
0.0	117	7	ADD70521	Add70521 Human sec
0.0	117	7	ADD39598	Add39598 Human sec
0.0	117	7	ADD70044	Add70044 Human sec
0.0	117	7	ADD37048	Add37048 Human sec
0.0	117	7	ADD38165	Add38165 Human sec
0.0	117	7	ADD39121	Add39121 Human sec
0.0	117	7	ADD3844	Add3844 Human sec
0.0	117	7	ADD40075	Add40075 Human sec
0.0	117	7	ADD50296	Add50296 Human sec
0.0	117	7	ADE19908	Ade19908 Human sec
0.0	117	7	ADE49819	Ade49819 Human sec

100000-0-US007377-
100000-0-US008439-
100000-0-US013358-
100000-0-US013705-
100000-0-US014042-
100000-0-US014941-
100000-0-US015264-
100000-0-US022031-
100000-0-US023522-
100000-0-US023328-
100000-0-US032678-
100000-0-US036052-
1000100-US017443-
1000100-US017800-
1000100-US019692-
1000100-US021056-
1000100-US021735-
1000100-US002797-

ECH INC.

Baker KP, Botstein DA, Deenoyers L, Eaton DL,
 Gao W, Gerber H, Gerritsen ME, Goddard A,
 Gurney AL, Klijaviv IJ, Mather JP, Napier MA, Pan J,
 Stewart TA, Tumas D, Watanabe CK, Williams PM;
 Ig Z; 96/47. 16.

4; 254pp; English.

and transmembrane PRO polypeptides, useful for treating
 ninal disorders and stimulating an immune response.

describes an isolated polypeptide (I) having at least 80
 quence identity to 30 secreted and transmembrane
 PRO polypeptides are also useful for stimulating
 adult heart, for inhibiting vascular endothelial growth
 tated proliferation of endothelial cells, stimulating
 of stimulated T-lymphocytes and for inducing proliferati
 eatic ductal cells and are thus useful in the treatment
 h involve protein secretion by the pancreas, including
 polypeptides are useful for inducing vascular permeability
 ng survival of retinal neurons and are thus useful
 ent of retinal disorders. PRO polypeptides are also usef
 g an immune response and inducing inflammation by induc
 11 and eosinophil infiltration at the site of infection
 PRO polypeptides are further useful for inducing apopto
 cells for inhibiting neoplastic growth. This is the am
 of a novel human secreted and transmembrane PRO polype

A

DT	28-MAY-2003	(first entry)
XX	DE	Novel human secreted and transmembrane protein PRO444.
XX	KW	Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO57; PRO337; PRO1411; PRO1095; PRO246; PRO603; PRO630; PRO635; PRO2630; PRO491; FGFR; biactive molecule; fibroblast growth factor receptor; cell death; chromosome mapping gene mapping; transgenic animal; knockout animal; gene therapy; t
XX	KW	obesity; diabetes; insulinemia; vascular permeability; cardiac insufficiency disorder; immune response; hearing loss; auditory hair cell regeneration; bone disorder; cartilage disorder sports injury; arthritis.
XX	KW	Homo sapiens.
XX	OS	US2003032063-A1.
XX	PN	13-FEB-2003.
XX	PP	01-FEB-2002; 20022US-00066494.
XX	PR	26-AUG-1997; 97US-0056974P. PR 17-SEP-1997; 97US-0059115P. PR 18-SEP-1997; 97US-0059263P. PR 19-SEP-1997; 97US-005958BP. PR 17-OCT-1997; 97US-006215P. PR 24-OCT-1997; 97US-0062816P. PR 24-OCT-1997; 97US-0063082P. PR 27-OCT-1997; 97US-0063329P. PR 29-OCT-1997; 97US-0063733P. PR 21-NOV-1997; 97US-0066364P. PR 25-NOV-1997; 97US-0066840P. PR 16-DEC-1997; 97US-0069644P. PR 09-FEB-1998; 98B1S-0074086P. PR 09-FEB-1998; 98B1S-00741092P. PR 25-MAR-1998; 98B1S-0079294P. PR 08-APR-1998; 98B1S-0081049P. PR 10-AUG-1998; 98B1S-0095998P. PR 18-AUG-1998; 98B1S-0097000P. PR 09-SEP-1998; 98B1S-0099600P. PR 10-SEP-1998; 98B1S-0099803P. PR 10-SEP-1998; 98B1S-0099811P. PR 14-SEP-1998; 98B1S-0099812P. PR 14-SEP-1998; 98BMO-US011933. PR 16-SEP-1998; 98BMO-US019330. PR 17-SEP-1998; 98B1S-01000858P. PR 17-SEP-1998; 98BMO-US019471. PR 24-SEP-1998; 98B1S-0101922P. PR 28-OCT-1998; 98B1S-0106032P. PR 20-NOV-1998; 98B1S-010930P. PR 20-NOV-1998; 98BMO-US024855. PR 25-NOV-1998; 98BMO-US025100. PR 01-DEC-1998; 98BMO-US019471. PR 08-MAR-1999; 99US-0050508P. PR 23-MAR-1999; 99US-0125778P. PR 01-SEP-1999; 99US-01020111. PR 02-JUN-1999; 99US-0102222. PR 15-JUN-1999; 99US-013969P. PR 20-JUL-1999; 99US-0145070P. PR 26-JUL-1999; 99US-014569P. PR 11-AUG-1999; 99US-014939P. PR 23-SEP-1999; 99US-015151P. PR 02-OCT-1999; 99US-015222P. PR 15-SEP-1999; 99US-01530P. PR 15-SEP-1999; 99US-0145070P. PR 30-SEP-1999; 99US-0145070P. PR 26-OCT-1999; 99US-014569P. PR 11-NOV-1999; 99US-014569P. PR 01-DEC-1999; 99US-014939P. PR 05-DEC-1999; 99US-0152856P. PR 07-DEC-1999; 99US-016949P. PR 20-DEC-1999; 99US-016949P. PR 05-JAN-2000; 99US-016949P. PR 18-FEB-2000; 2000US-0000239. PR 18-FEB-2000; 2000US-000442. PR 18-FEB-2000; 2000US-000442.

sequences defined in the specification (or encoding the mature protein or a PRO protein extracellular domain), a PRO expression vector comprising the vector, PRO fusion proteins, anti-PRO antibodies and a method for linking a bioactive molecule to a cell expressing the above PRO polypeptides, the bioactive molecule is radiolabel or an antibody and causes the death of the cell. PRO C antibody is useful for modulating at least one biological activit C cell expressing the above polypeptides. PRO is useful for identif C agonists or antagonists of PRO, for preparing a variant of PRO, a C molecular weight markers for protein electrophoresis purpose and C nucleic acid is useful for recombinantly expressing those markers C also useful as therapeutic agent. PRO is useful in assays to iden C other proteins or molecules involved in binding interaction. PRO C acid is useful as hybridisation probes, in chromosome and gene ma C in generation of antisense RNA and DNA, in the preparation of PRO C polypeptide, in gene therapy, for generating transgenic animals o C knockout animals which in turn are useful in the development and C screening of therapeutically useful reagents, to construct hybrid C probes for mapping the gene which encodes the PRO and for the gen C analysis of individuals with genetic disorders, for chromosome C identification, as a chromosome marker, and for generating probes C polymerase chain reaction (PCR), Northern analysis, Southern anal C Western analysis. The antibody is useful in diagnostic assays for C e.g. detecting its expression in specific cells, tissues or serum C affinity purification of PRO from recombinant cell culture or nat C sources. PRO or Ab is useful for the preparation of medicament or C treating condition which is responsive to the PRO polypeptide or C PRO antibody. PRO and PRO nucleic acid are useful for tissue typi C present sequence encodes a PRO polypeptide

CH INC., Baker KP, Botstein DA, Desnoyers L, Eaton DL,
Gao J, Gerber H, Gerritsen MB, Goddard A;
Kljanine AL, Mather MA, Napier MA;
Larney AL, Mathur JU, Pan J;
Stewart TA, Tumas D, Watcombe CK, Williams PM;

11

Baeker KP., Botstein DA., Desnoyers L., Eaton DL., Goddard A., Gerritsen MB., Gerber H., Kjærneby J., Kljærneby AL., Mathur JP., Napier MA., Pan J., Parmenter R., Stewart TA., Tumanski CK., Williams PM.

ABU33383;

17-SEPB-2003 (Fixer enter)

17-CEP-201

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201

1

belated to an isolated, secreted/transmembrane polypeptide, having at least 80% sequence identity to a sequence encoded by any one of the 37 sequences appearing as ABU77 in the ATCC numbers given in the specification. Also, to a sequence selected from any one of the 37 CDNA

200111S-00015869

:000WO-US014941.
:000WO-US015234.
:000WO-US023322.
:000WO-US023328.
:000WO-US030932.
:000WO-US030873.
:000WO-US032678.
:001WO-US006520.
:001WO-US006666.
:001WO-US017890.
:001WO-US019692.
:001WO-US021066.
:001WO-US021735.
:001US-00946374.

TECH INC.

:stein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
d A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
Wood WI;

:93/55.

:42.

1 PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,
modulate glucose or free fatty acid uptake by skeletal
and are useful for treating diabetes, hyper- or hypo-

urity 100.0%; Score 609; DB 6; Length 117;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

:WAVFLASRLSGQILLTLEHIAHFLGIGGGAAATTMGNSICIDDDSGCDSDVDTQQ 60

:WAVFLASRLSGQILLTLEHIAHFLGIGGGAAATTMGNSICIDDDSGCDSDVDTQQ 60

:SAVPTADRSQPRDPVPRPDRPVRPRRGPGHPRRKCONVTDLVPLAVRTLVDK 117

:SAVPTADRSQPRDPVPRPDRPVRPRRGPGHPRRKCONVTDLVPLAVRTLVDK 117

E.D.

lard; protein; 117 AA.

first entry)

/transmembrane polypeptide PRO44.

d protein; transmembrane protein; PRO; VEGF inhibitor;
helial growth factor; endothelial cell proliferation;
proliferation; endothelial cell apoptosis;
ion; pancreatic beta cell differentiation,
oliferation; glucose uptake; free fatty acid; FFA uptake;

:1.

:002US-00066211.
97US-0056974P.
97US-0059233P.
97US-0059588P.
97US-0062283P.
97US-0062816P.

(GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;

PN	US2003044841-A1.
XX	
PD	06-MAR-2003.
XX	
PF	06-DEC-2001; 2001US-00006856.
XX	
PR	01-SEP-1998; 98US-0098716P.
PR	01-SEP-1998; 98US-0098723P.
PR	01-SEP-1998; 98US-0098749P.
PR	01-SEP-1998; 98US-0098750P.
PR	02-SEP-1998; 98US-0098821P.
PR	02-SEP-1998; 98US-0098843P.
PR	09-SEP-1998; 98US-0098563P.
PR	09-SEP-1998; 98US-0098596P.
PR	09-SEP-1998; 98US-0098602P.
PR	09-SEP-1998; 98US-0098642P.
PR	10-SEP-1998; 98US-0098741P.
PR	10-SEP-1998; 98US-0098754P.
PR	10-SEP-1998; 98US-0098763P.
PR	10-SEP-1998; 98US-0100385P.
PR	15-SEP-1998; 98US-0100388P.
PR	15-SEP-1998; 98US-0100519P.
PR	16-SEP-1998; 98US-0100584P.
PR	16-SEP-1998; 98US-0100627P.
PR	16-SEP-1998; 98US-0100611P.
PR	16-SEP-1998; 98US-0100662P.
PR	17-SEP-1998; 98US-0100644P.
PR	17-SEP-1998; 98US-0100684P.
PR	17-SEP-1998; 98US-0100710P.
PR	17-SEP-1998; 98US-0100919P.
PR	17-SEP-1998; 98US-0100930P.
PR	18-SEP-1998; 98US-0100849P.
PR	18-SEP-1998; 98US-0101014P.
PR	18-SEP-1998; 98US-0101068P.
PR	18-SEP-1998; 98US-0101071P.
PR	23-SEP-1998; 98US-0101471P.
PR	23-SEP-1998; 98US-0101472P.
PR	23-SEP-1998; 98US-0101473P.
PR	23-SEP-1998; 98US-0101474P.
PR	23-SEP-1998; 98US-0101475P.
PR	23-SEP-1998; 98US-0101476P.
PR	23-SEP-1998; 98US-0101477P.
PR	23-SEP-1998; 98US-0101479P.
PR	23-SEP-1998; 98US-0101479P.
PR	24-SEP-1998; 98US-0101741P.
PR	24-SEP-1998; 98US-0101743P.
PR	24-SEP-1998; 98US-0101915P.
PR	24-SEP-1998; 98US-0101916P.
PR	29-SEP-1998; 98US-0102240P.
PR	29-SEP-1998; 98US-0102307P.
PR	29-SEP-1998; 98US-0102330P.
PR	29-SEP-1998; 98US-0102331P.
PR	30-SEP-1998; 98US-0102484P.
PR	30-SEP-1998; 98US-0102487P.
PR	30-SEP-1998; 98US-0102570P.
PR	30-SEP-1998; 98US-0102571P.
PR	01-OCT-1998; 98US-0102684P.
PR	01-OCT-1998; 98US-0102687P.
PR	02-OCT-1998; 98US-0102965P.
PR	06-OCT-1998; 98US-0103258P.
PR	06-OCT-1998; 98US-0103449P.
PR	07-OCT-1998; 98US-0103314P.

(First entry)

d/transmembrane protein PRO444.
ed protein; transmembrane protein; PRO; vulnerability; cardiot;

anorectic; antiarthritic; angiogenesis; cancer; cell capillary; endothelial; epithelial; growth; wound healing; lymphocyte proliferation; immune response suppression; hypertension; hypotension; hypoxia; insulin resistance; insulin; insulinoma; diabetes; obesity; or hyperinsulinaemia; differentiation; bone disorder; cartilage disorder; arthritis.

980US-0104987P;
980US-0105000P;
980US-0105000P2P;
980US-01050104P;
980US-0105104P;
980US-01052169P;
980US-01052266P;
980US-0105693P;
980US-0105694P;
980US-0105807P;
980US-0105881P;
980US-0105882P;
980US-0106062P;
980US-0106023P;
980US-0106029P;
980US-0106030P;
980US-0106032P;
980US-0106033P;
980US-0106384P;
980US-01067178P;
980US-0106248P;
980US-0106384P;
980US-0106854P;
980US-0106464P;
980US-0106856P;
980US-0106902P;
980US-0106905P;
980US-0106932P;
980US-0106934P;
980US-0106934P;
980US-01069735P;
980US-01069806P;
980US-0106987P;
980US-01069878P;
980US-01069925P;
980US-0107887P;
980US-0108001P;
980US-0108001P;
980US-01080783P;
980US-01080849P;
980US-01080849P;
980US-0108086P;
980US-0108087P;
980US-010808852P;
980US-010808858P;
980US-01080904P;
980US-0108281351;
980US-0113296P;
980US-0114223P;
990US-00010106;
990US-002844291;
990US-0126764P;
990US-0141037P;
990US-0147598P;
990US-0145698P;
990US-00010111;
990US-00013707;
990US-00137097;
990US-00137097;
990US-00137097;

0000W-	US023328
0000W-	US030952
0000W-	US030873
0000W-	US032678
001W-	US006520
001W-	US006666
001US-	US0872035
001US-	US017800
001US-	US0882636
001W-	US019692
001W-	US210735
001W-	US021735

TECH INC.

Wood W1

PRO polypeptides e.g. PRO1491 and PRO1571, useful in the treatment of a condition responsive to PRO and as therapeutic agents e.g. vaccines.

A : 561nn : English

describes an isolated PRO (secreted and transmembrane) having at least 80% sequence identity to a sequence

Score 609; DB 7; Length 117;

nservative 0; *Mismatches* 0; *Indels* 0; *Gaps* 0;

WAVFLASRSLGQGLLITTLEHIAHFLGTGGAAATTMGNNSCICRDDSGTDDSVDTQQ 60

WAVFLASRSILQGMLLTLIEHIAHFLGTGGAAATTMGNNSCICRDGSCTDDSVDTQQ 60

ISAVPTADTRSOPRDPVVRPPRRGRGPHEPRRKQNVGLVLDLAVIRTLVDK 117

ISAVPTADTRSQPRDFVRPFRGRGPHEPRKKQNVGGLVLDLAVRLVDK 117

卷之三

THESE ARE THE WORDS OF JESUS CHRIST

β -transmembrane protein PRO444.

secreted and transmembrane protein; gene therapy; gene transfer

:inocyte differentiation; psoriasis; epithelial cancer;

arterial sclerosis; inflammatory disease; organ failure;

{ birth defect; premature aging; AIDS; cancer;

PR 28-FEB-2001 / 2001WO-US0006520.
 PR 30-MAY-2001 / 2001WO-US017443.
 PR 01-JUN-2001 / 2001WO-US017800.
 PR 20-JUN-2001 / 2001WO-US019692.
 PR 29-JUN-2001 / 2001WO-US021066.
 PR 09-JUL-2001 / 2001WO-US02135.
 PR 15-NOV-2001 / 2001US-00002796.
 XX
 2002US-000066193.
 Q71C-005697AD

TECH TNC

Baker KP, Botstein DA, Desnoyers L, Eaton DL,
Gong S, Gao W, Gerber H, Goddard A,
Gurley AL, Klarin IJ, Gerritsen ME,
Mather JP, Napier MA, Pan J,
Nayyar MA, Stewart TA, Tunas D, Watanaabe CR,
Williams PM;

ng Z;
261/46.
202.

peptides and nucleic acid molecules, useful in diagnosing cardiovascular diseases, organ failure, atherosclerosis, carditis, inflammatory diseases, Alzheimer's disease or Parkinson's disease, AIDS, cancer.

4 : 154pp; English.
relates to an isolated native sequence PRO polypeptide transmembrane protein) having 80% sequence similarity to transmembrane sequences (or PRO lacking signal peptide, a PRO domain (with or without a signal peptide) encoded by a 80% identical to one of 37 cDNA sequences), shown in the cells comprising the vectors used to produce the PRO nucleic acid sequence, an anti-PRO antibody, linking a nucleic acid sequence to a cell expressing the PRO polypeptides and least one biological activity of a cell expressing the PRO polypeptides and nucleic acids are useful in treating enterocolitis, gastrointestinal ulceration, skin triciated with abnormal keratinocyte differentiation, e.g., epithelial cancers such as squamous cell carcinoma, diseases, Parkinson's disease, amyotrophic lateral sclerosis, e.g. rheumatoid arthritis, asthma or multiple sclerosis, heart failure, atherosclerosis, cardiac injury, infertility, premature aging, AIDS, cancer, diabetic complications, or general. The polypeptides are also useful for wound repair and therapies concerned with re-growth of tissue. The sequences may be used as hybridization probes in chromosome mapping, or in generating antisense RNA and DNA. PRO nucleic acid useful in preparing PRO polypeptides, in assays to determine proteins or molecules involved in binding reaction, to isogenic animals or knockout animals, which in turn are useful development and screening of therapeutically useful reagents, for identification, and tissue typing. The PRO polypeptides and molecules are also useful in gene therapy, and as molecular for protein electrophoresis purposes. The anti-PRO may be used in diagnostic assays for PRO, or for the affinity of PRO in recombinant cell culture or natural sources. The

AA; AA; AA; AA; AA;

AA	Amino Acid	Score	DB	Length
arity	100.0%	609	7	117
on servative	100.0%	Prod. No.	2e-63	
		Mismatches	0	
		Indels	0	
		Gaps	0	

GMWAVFLASRSLGQGLLTLLEBHAIFLGTGGAATTMGNSC1C RD SGTDVQQ 60
GMWAVFLASRSLGQGLLTLLEBHAIFLGTGGAATTMGNSC1C RD SGTDVQQ 60
GNSA NSAVPTADPSQPRDPPRGPGRGPHEPRKQNDGLVLDITLA VIRTLYDK 117

NSAVPTADRSQPRDPVVRPVR

PR	15-SSP-1939;	99W0-US021194;	
PR	29-OCT-1939;	99US0-0162506P.	
PR	30-NOV-1939;	99W0-US028313.	
PR	02-DEC-1939;	99W0-US028551.	
PR	16-DEC-1939;	99W0-US030095.	
PR	05-JAN-2000;	2000W0-US000219.	
PR	06-JAN-2000;	2000W0-US000376.	
PR	11-FEB-2000;	2000W0-US003565.	
PR	18-FEB-2000;	2000W0-US004342.	
PR	24-FEB-2000;	2000W0-US005004.	
PR	02-MAR-2000;	2000W0-US005841.	
PR	15-MAR-2000;	2000W0-US006884.	
PR	17-MAY-2000;	2000W0-US013705.	
PR	22-MAY-2000;	2000W0-US014042.	
PR	30-MAY-2000;	2000W0-US014941.	
PR	02-JUN-2000;	2000W0-US015264.	
PR	23-JUN-2000;	2000W0-US023522.	
PR	24-AUG-2000;	2000W0-US023328.	
PR	08-NOV-2000;	2000W0-US030952.	
PR	10-NOV-2000;	2000W0-US030873.	
PR	01-DEC-2000;	2000W0-US031678.	
PR	28-FEB-2001;	2001W0-US006520.	
PR	01-MAR-2001;	2001W0-US006666.	
PR	01-JUN-2001;	2001W0-US017800.	
PR	20-JUN-2001;	2001W0-US019692.	
PR	29-JUN-2001;	2001W0-US021066.	
PR	09-JUL-2001;	2001W0-US021735.	
PR	04-SEP-2001;	2001W0-US046374.	
XX	(GETH) GENENTECH INC.	PA	
XX	Baker KP, Borstein D, Desnoyers L, Eaton DL, Ferrara N, Fong Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillia Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Wata Williams PM, Wood WI;		
PS	WPI; 2003-555602/52.		
DR	N-PSNBB; ADC17874.		
XX	Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful preparation of a medicament for treating a condition responsive to PT polypeptide, and as therapeutic agents e.g. vaccines.		
PS	Claim 12; SEQ ID NO 6; 55PP; English.		
CC	The invention relates to human PRO polypeptides and the polynucleic acid encoding them. The sequences are useful in the preparation of a medicament for treating a condition responsive to a PRO polypeptide. PRO polypeptides are useful in a number of functional biological assays molecular weight markers for protein electrophoresis and as therapy.		
XX			
PS	Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 11; Length 117; Pred. No. 2e-63; Mismatches 0; Indels 0; G		
CC			
Qy	1 MIVFGWAVFLASRSLGGQLLTLFEHTAHFLCTGGAAATTMGNSCICDDSGCTDDSV		
Db	1 MIVFGWAVFLASRSLGGQLLTLFEHTAHFLCTGGAAATTMGNSCICDDSGCTDDSV		
Qy	61 QQAENSAVPTADRSQDPDVRPFRGRGPHEPRRKCONVGDVLDFIAVRLVLD		
Db	61 QQAENSAVPTADRSQDPDVRPFRGRGPHEPRRKQNVDLGLVDTLAVRLVLD		
XX	RESULT 13 ADD10295 ID ADD10295 standard; protein: 117 AA.		
XX	ADD10295; AC ADD10295;		
XX	01-JAN-2004 (first entry)		
XX	Human Secreted Transmembrane PRO domain peptide #1		

first entry
 /transmembrane protein PRO444.
 d protein; transmembrane protein; PRO; tumour;
 e; cardiac insufficiency disorder; calcium flux;
 ; endothelial cell; bone disorder; cartilage disorder;
 and healing; diabetes; skeletal muscle cells; obesity;
 ; nephropathy; Schonlein-Henoch purpura; coeliac disease;
 ; retiformis; Crohn's disease; thalassaemia.
 .1.
 :001US-00015386.

PR 24-SEP-1998; 98US-0101916P.
 PR 29-SEP-1998; 98US-0102240P.
 PR 29-SEP-1998; 98US-0102440P.
 PR 29-SEP-1998; 98US-0102330P.
 PR 29-SEP-1998; 98US-0102331P.
 PR 30-SEP-1998; 98US-0102484P.
 PR 30-SEP-1998; 98US-0102487P.
 PR 30-SEP-1998; 98US-0102510P.
 PR 30-SEP-1998; 98US-0102571P.
 PR 01-OCT-1998; 98US-0102684P.
 PR 01-OCT-1998; 98US-0102687P.
 PR 02-OCT-1998; 98US-010265P.
 PR 06-OCT-1998; 98US-0103258P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 07-OCT-1998; 98US-0103115P.
 PR 07-OCT-1998; 98US-0103128P.
 PR 07-OCT-1998; 98US-0103195P.
 PR 07-OCT-1998; 98US-0103396P.
 PR 07-OCT-1998; 98US-0103410P.
 PR 08-OCT-1998; 98US-0103633P.
 PR 08-OCT-1998; 98US-0103678P.
 PR 08-OCT-1998; 98US-0103679P.
 PR 14-OCT-1998; 98US-0104357P.
 PR 20-OCT-1998; 98US-0104987P.
 PR 20-OCT-1998; 98US-0105000P.
 PR 20-OCT-1998; 98US-0105002P.
 PR 21-OCT-1998; 98US-0105104P.
 PR 22-OCT-1998; 98US-0105169P.
 PR 22-OCT-1998; 98US-0105466P.
 PR 26-OCT-1998; 98US-010563P.
 PR 26-OCT-1998; 98US-0105634P.
 PR 27-OCT-1998; 98US-0105607P.
 PR 27-OCT-1998; 98US-0105882P.
 PR 27-OCT-1998; 98US-0105882P.
 PR 27-OCT-1998; 98US-0106062P.
 PR 28-OCT-1998; 98US-0106023P.
 PR 28-OCT-1998; 98US-0106029P.
 PR 28-OCT-1998; 98US-0106030P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 28-OCT-1998; 98US-0106033P.
 PR 28-OCT-1998; 98US-0106178P.
 PR 29-OCT-1998; 98US-0106248P.
 PR 29-OCT-1998; 98US-0106330P.
 PR 30-OCT-1998; 98US-0106465P.
 PR 03-NOV-1998; 98US-010656P.
 PR 03-NOV-1998; 98US-0106502P.
 PR 03-NOV-1998; 98US-0106505P.
 PR 03-NOV-1998; 98US-0106919P.
 PR 03-NOV-1998; 98US-0106932P.
 PR 03-NOV-1998; 98US-0106934P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 17-NOV-1998; 98US-0108775P.
 PR 17-NOV-1998; 98US-010887P.
 PR 17-NOV-1998; 98US-0108867P.
 PR 17-NOV-1998; 98US-0108878P.
 PR 17-NOV-1998; 98US-0108925P.
 PR 18-NOV-1998; 98US-0108801P.
 PR 18-NOV-1998; 98US-0108849P.
 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108904P.
 PR 22-DEC-1998; 98US-0113296P.

14:34:39 2004

us-10-066-273-9.rag

1

98US-0114223P.
99NO-US000106.
99TS-US0128674P.

99TS-01141037P.
99US-01144758P.

99US-01145698P.
99NO-US020111.

99US-01021194.
99US-0162506P.

99NO-US028313.
99NO-US028551.

99NO-US010095.
2000NO-US000219.

2000NO-US000376.
2000NO-US003565.

2000NO-US004342.
2000NO-US005004.

2000WO-US05841.

2000WO-US006884.

2000NO-US013705.
2000NO-US014042.

2000NO-US014941.
2000NO-US015264.

2000WO-US03522.

2000NO-US023328.
2000NO-US030952.

2000NO-US032073.
2000NO-US02678.

2001WO-US006520.
2001NO-US00666.

2001WO-US017800.
2001WO-US019692.

2001WO-US021066.
2001US-00946374.

520.

DECH INC.

Stein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
rd A, Godowski PJ, Grimaldi JC, Gurley AL, Hillan KJ;
NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
Wood WI;

602/81.

520.

¹ PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555,
to glucose or free fatty acid (FFA) uptake by skeletal muscle
useful for treating diabetes or hyper- or hypo-insulinemia.

ID NO 6: 553pp; English.

relates to an isolated PRO polypeptide (secreted or

arity 100.0%; Score 609; DB 7; Length 117;
conservative 100.0%; Pred. No. 2e-63; Mismatches 0; Indels 0; Gaps 0;

3WAVFLASRSIIGQGLLTLREHIAFLGIGGAAATMGNSTICRDSGTDSSVDTQQ 60
3WAVFLASRSIIGQGLLTLREHIAFLGIGGAAATMGNSTICRDSGTDSSVDTQQ 60

NSAVPTADTRSQPRDPRVRPRRGGRGPHEPRRKKCONVGDGLVLDTLAVITLVDK 117
NSAVPTADTRSQPRDPRVRPRRGGRGPHEPRRKKCONVGDGLVLDTLAVITLVDK 117

April 2, 2004, 10:24:42

362
JRC

Copyright GenCore version 5.1.6
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In search, using bw model

at 2, 2004, 10:12:49 ; Search time 17 Seconds
(without alignments)
358,365 Million cell updates/sec

10-066-273-9
1IVFGWAVFLASRSLGQGII.....QNVDGLVDTLAVITLVDK 117

STIM62

OP 10.0 , Gapext 0.5

.681 seqs, 52070155 residues

satisfying chosen parameters:

141681

ith: 0

ith: 2000000000

nimum Match 0%

maximum Match 100%

string first 45 summaries

missProt_42::

the number of results predicted by chance to have a
than or equal to the score of the result being printed,
d by analysis of the total score distribution.

SUMMARIES

TRY	Length	DB	ID	Description
1.0	612	1	THIC_STRCO	-
1.9	188	1	SSB_ALCEU	Q9X9u0 streptomyce
1.8	1483	1	BAB_HUMAN	P59927 alcaligenes
1.3	286	1	MSA2_PLAF1	Q9ui90 homo sapien
1.1	2505	1	CCAA_HUMAN	P50496 plasmidium
1.0	281	1	TGN1_PLAFH	Q00555 homo sapien
1.0	353	1	TGN1_MOUSE	Q92319 plasmidium
1.0	1466	1	CA13_HUMAN	Q02461 homo sapien
1.9	262	1	MSA2_PLAFC	Q99317 plasmidium
1.9	272	1	MSA2_PLAF7	P50498 plasmidium
1.9	274	1	MSA2_PLAF6	P50497 plasmidium
1.9	287	1	MSA2_PLAFG	P19260 plasmidium
1.9	300	1	MSA2_PLAFI	Q03644 plasmidium
1.9	300	1	MSA2_PLAFZ	Q03645 plasmidium
1.9	302	1	MSA2_PLAF9	Q03994 plasmidium
1.9	347	1	MSA2_PLAF2	Q03646 plasmidium
1.9	458	1	YNE31_CAEEL	P30640 caenorhabdi
1.8	1787	1	CHD3_CAEEL	Q2516 caenorhabdi
1.7	1479	1	BAB_MOUSE	Q9z277 mus musculu
1.6	3726	1	TRX_DRONE	P20659 drosophila
1.5	445	1	NR33_MOUSE	Q9z0Y9 mus musculu
1.3	1944	1	CHD3_HUMAN	Q12873 homo sapien
1.2	424	1	COT1_BOVIN	Q9tr8 bos taurus
1.2	445	1	NR33_RAT	Q62685 ratus norv
1.2	504	1	FTSY_SYN3	P73930 synochocyst
1.2	702	1	EXO1_YEAST	P39875 saccharomyces
1.1	399	1	SIR3_HUMAN	Q9nt97 homo sapien
1.1	727	1	CTCF_HUMAN	P49711 homo sapien
1.1	1208	1	IC14_HSV1	P08392 herpes simp
1.0	393	1	CT14_HUMAN	Q9nyg8 homo sapien
1.0	1202	1	NOS3_HUMAN	P29474 homo sapien
1.0	3828	1	TRX_DRONI	Q24742 drosophila
1.9	217	1	YKR4_EBV	P30117 epstein-bar

ALIGNMENTS

RESULT 1
THIC_STRCO
ID THIC_STRCO
AC Q9X9u0;
STANDARD;
PRT; 612 AA.
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Thiamine biosynthesis protein thiC.
GN THIC OR SCO3928 OR SQU1.11.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Streptomyces; Streptomyctaceae; Streptomyces.
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=A3 (2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.P., Cardeno-Tarraga A.-M., Challis G.I.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Oliver K., O'Neill S.,
RA Rabbinowitch E., Rajandream M.A., Rutherford K., Murphy L.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor J.,
RA Warren T., Wietzorek A., Woodward R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete Genome sequence of the model actinomycete Streptomyces
coelicolor A3 (2)." ;
RL Nature 417:141-147 (2002).
CC :- FUNCTION: Required for the synthesis of the hydromethyl-5'-
CC (HMP) moiety of thiamine (4-amino-2-methyl-5'-
CC hydroxymethylpyrimidine) (By SIMILARITY).
CC :- PATHWAY: Thiamine biosynthesis.
CC :- SIMILARITY: Belongs to the thiC family.
CC This SWISS-PROT entry is copyright. It is produced through a coll:
CC between the Swiss Institute of Bioinformatics and the EMBL out:
CC the European Bioinformatics Institute. There are no restriction:
CC use by non-profit institutions as long as its content is in
CC modified and this statement is not removed. Usage by and for c:
CC entities requires a license agreement (See http://www.isb-sib.ch/).
CC or send an email to license@isb-sib.ch).

EMBL: AL939118; CAB46966-1; -.
CC InterPro: IPR0217; T37181; T37181.
DR HAMAP; MF_00089; -; 1.
DR InterPro: IPR0217; ThiC.
DR Pfam; PF01964; ThiC; 1.
DR ProDom; PDD07048; ThiC; 1.
DR TIGRFAMs; TIGR00190; thiC; 1.
KW Thiamine biosynthesis; Complete proteome.
SQ SEQUENCE 612 AA; 67371 MW; 2908F245/2000CP68 CRC64;

Query Match Score 79; DB 1; Length 612;
Best Local Similarity 31.0%; Pred. No. 2.4;
Matches 30; Conservative 31.2%; Mismatches 7; Indels 22; Gi

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pe, alpha-1 polypeptide isoform 4) (Brain calcium channel CACNA1A4 OR CACH4 OR CACN3).
 (Human);
 Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Primates; Catarrhini; Hominidae; Homo.
 [66];

1 N.A. (ISOFORMS BI-1-GGCAG/1A-1 AND BI-1/1A-2);
 1614; PubMed=1049321;
 Itia A., Deal C., Brust P.F., Stauderman K., Ellis S.B., Johnson E.C., Williams M.E.;
 Elements in domain IV that influence biophysical and
 al properties of human alpha1A-containing high-voltage-
 calcium channels.";
 6:1384-1400(1999).

1 N.A. (ISOFORM BI-1(V1)), AND VARIANTS FHM.
 1792; PubMed=898806;
 Terwindt G.M., Vergouwe M.N., van Eijk R., Oefter P.J., Lamerdin J.E., Mohrenweiser H.W., Bulman D.E., Liang J., Lindhout D., van Ommen G.-J.B., Hofker M.H., Frants R.R.;
 episodic migraine and episodic ataxia type-2 are caused by the Ca2+ channel gene CACNA1A4.";
 52(1996).

1 N.A., AND ALTERNATIVE SPLICING.
 920; PubMed=8988170;
 Bailey J., Bonnen P.E., Abizayava T., Stockton D.W., Wains W.B., Subramony S.H., Zoghbi H.Y., Lee C.C.;
 dominant cerebellar ataxia (SCA6) associated with small expansions in the alpha 1A-voltage-dependent calcium channel gene.
 5:62-69(1997).

.231-1651 FROM N.A., McCreadie P.M., Skowronski E., Adamson A.W., Ultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S., Esco N., Do L., Recala W., Terry A., Garnes J., Poundstone P., Christensen M., Georgescu A., Avila J., C., Andreise T., Frankheim M., Amico-Keller G., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Arellano A., Montgomery M., Ow D., Nolan M., Trong S., Olsen A.S., Carrano A.V.;
 15:274-283(1995).

693-1807 FROM N.A.
 419; PubMed=7823133;
 Vigliano M.P., Kim Y.I., Froehner S.C.;
 und antibody inhibition of P-type calcium channels in cell lung carcinoma cells."/

:038-2258 FROM N.A.
 310; PubMed=8525133;
 Breschler T.S., Li S.H., Kidwai A.S., Antonarakis S.E., Ross C.A.;
 15:274-283(1995).

CC are blocked by the funnel toxin (Ftx) and by the omega-agatoxin IVA (omega-Aga-IVA). They are however insensitive to dihydropyridines (DHP), and omega-conotoxin-GVIA (omega-CTx-1).

CC -!- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUIT IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DE LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- ALTERNATIVE PRODUCTS:

CC Comment=Additional isoforms seem to exist;

CC Name=BI-1-GGCAG; Synonyms=1A-1;

CC IsoId=000555-1; Sequence=Displayed;

CC Name=BI-1(V1); Sequence=VSP_000875;

CC IsoId=000555-2; Sequence=VSP_000875;

CC Name=BI-1(V1); Sequence=VSP_000871; VSP_000875;

CC IsoId=000555-3; Sequence=VSP_000871;

CC IsoId=000555-4; Sequence=VSP_000871;

CC Name=BI-1(V2);

CC IsoId=000555-5; Sequence=VSP_000872;

CC Name=BI-1(V2); Sequence=VSP_000872;

CC IsoId=000555-6; Sequence=VSP_000872;

CC Name=BI-1(V2,V3);

CC IsoId=000555-7; Sequence=VSP_000873; VSP_000874;

CC -!- TISSUE SPECIFICITY: Brain specific; mainly found in cerebellar cortex, thalamus and hypothalamus. No expression in heart, kidney, liver or muscle. Purkinje cells contain predominantly P-type VSCC, the Q-type being a prominent calcitonin receptor.

CC -!- DOMAIN: Each of the four internal repeats contains five hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and probably represent the voltage-sensor and are characterized by positively charged amino acids at every third position.

CC -!- POLYMORPHISM: The poly-Gln region of CACNA1A is polymorphic; 17 repeats in the normal population, expanded to about 21 to repeats in spinocerebellar ataxia 6 (SCA6) patients. There seems to be a correlation between the repeat number and earlier onset of the disorder.

CC -!- DISEASE: Defects in CACNA1A are the cause of spinocerebellar ataxia type 6 (SCA6) [MIM:183086]. SCA6 is an autosomal dominant disorder characterized by slowly progressive cerebellar atrophy, the limbs and gait, dysarthria, nystagmus, and mild vibrator proprioceptive sensory loss. These symptoms are probably explained by severe loss of cerebellar Purkinje cells. SCA6 is caused by expansion of a CAG repeat in the coding region of CACNA1A.

CC -!- DISEASE: Defects in CACNA1A are the cause of familial hemiplegic migraine (FHM) [MIM:141500]; also known as migraine familial hemiplegic 1 (MHP1). FHM, a rare autosomal dominant subtype of migraine with aura, is associated with ictal hemiparesis and some families, progressive cerebellar atrophy.

CC -!- DISEASE: Defects in CACNA1A are the cause of episodic ataxia 2 (EA2) [MIM:108500]; also known as acetazolamide-responsive hereditary paroxysmal cerebellar ataxia (APCA). This autosomal dominant disorder is characterized by acetazolamide responsiveness, attacks of cerebellar ataxia and migraine-like symptoms, interictal nystagmus, and cerebellar atrophy.

CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.

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MSA2.
Plasmodium falciparum (isolate thtn / Thailand);
Plasmodium; Alveolata; Apicomplexa; Haemosporida; Plasmoidium.
NCBI_TaxID=70151;
[1]
SEQUENCE FROM N.A. MEDLINE=91218803; PubMed=2030943;
Thomas A.W.; Carr D.A.; Carter J.M.; Lyon J.A.;
"Sequence comparison of allelic forms of the Plasmodium falciparum
merozoite surface antigen MSA2.";
Mol. Biochem. Parasitol. 43:211-220 (1990).
- I - FUNCTION: May play a role in the merozoite attachment to the
erythrocyte.
- I - SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
(potential).
- I - DEVELOPMENTAL STAGE: During the trophozoite and schizont stag

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entities requires a license agreement (See <http://www.isb-sib.ch/>
or send an email to license@isb-sib.ch).

EMBL; M60189; AAA29689; 1; -.
InterPro; IPR001136; MSA_2.
PFam; PF00985; MSA_2; 1.
Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
GPI-anchor; Merozoite;
GPI-anchor; Merozoite;
SIGNAL 1 20 POTENTIAL.
CHAIN 21 257 MEROZOITE SURFACE ANTIGEN 2.
PROPEP 258 281 HYDROPHOBIC, REMOVED DURING MATURATION
(BY SIMILARITY).
DOMAIN 44 207 POLYMORPHIC REGION.
DOMAIN 111 118 POLY-THR.
CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 158 158 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 230 230 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 254 254 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 255 255 N-LINKED (GLCNAC. .) (POTENTIAL).
SEQUENCE 281 AA; 28892 MW; 50598AA42D64CCBC CRC64;
Query Match 12.0%; Score 73; DB 1; Length 281;
Best Local Similarity 35.8%; Pred. No. 4;
Matches 24; Conservative 6; Mismatches 25; Indels 12; G.
36 AATTMGNSCICRDSGTDSV-----DT-----QQQZQENSAAVTADTSQPRDP
152 ANTTETONNSNVQODSQTKSNVPPTQDADTKSPTAQEQAENSA-PTAEQTESPELQ:
85 RGRGRGPH 91
211 NKGTGQH 217

SU117
N1_MOUSE TGN1_MOUSE STANDARD; PRT; 353 AA.
Q62313;
15-MAR-2004 (Rel. 4.3, Created)
15-MAR-2004 (Rel. 4.3, Last sequence update)
15-MAR-2004 (Rel. 4.3, Last annotation update)
TG0NL1 OR TTG0NL1
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Buteraria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=ICR; TISSUE=Brain;

N.A.

270:14471-14476 (1995).

253; PubMed=7540170;

ahashi S., Murakami K., Nakayama K.;
EC presence of two TGN38 isoforms and absence of TGN41

255; TISSUE=Aorta, and Testis;
PubMed=12466851;

arunno M., Kasukawa T., Adachi J., Bono H., Kondo S., Kiyosawa H.,
sato N., Saito R., Suzuki H., Yamakawa I., Yonemoto A., Gajobori T.,
Yamada Y., Hasegawa Y., Nagami A., Schonbach C., Gajobori T.,
Hill D.P., Bult C., Humm D.A., Quackenbush J.,
Korpi K., Batalov S., Beisel K.W.,
Kroenert D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
Gani T.A., Flitcher C.P., Forrest A., Frazer K.S.,
Garibaldi M., Gissi C., Godzik A., Gough J.,
Gustincovich S., Hirokawa N., Jackson J.J., Jarvis E.D.,
Kajiji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maltais L., Marchionni L., McKenzie L., Miki H.,
Numata K., Okido T., Pavian W.J., Peretea G., Pabo G.,
Pilla R., Ponticelli U., Qi D., Ramachandran S.,
Reed J.C., Reed D.J., Reid J., Ringwald M.,
Schneider C., Semple C.A., Setou M., Shimada K.,
Shigenaka T., Taylor M.S., Teasdale R.D., Tomita M.,
Schnapf L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
Yan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
Yoshikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
Yanagi K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
Imotani K., Ishii Y., Itoh M., Kagawa I.,
Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Yoshino M., Waterston R., Lander E.S., Rogers J.,
Ashizaki Y.

The mouse transcriptome based on functional annotation of
long cDNAs. ;

3-573 (2002).

23571 PubMed=12477932;

Feingold E.A., Grouse L.H., Derge J.G.,

Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

N.K., Bhaet C.P., Schaeter R.H., Buettow B., Zeeberg T.

Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.

J.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Queliano N.A., Peters G.J., Abramson R.D., Mullahy S.J.

MUSZNY D. M., Södergren E. J., Lu X., Gibbs R. A.

ton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.

Sadan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Touchman J.W., Green E.D., Dickson M.C., Griswold T., Schmitz T., Myers B.M.

Schein J.E., Jones S.J.M., Marr M.A.

and initial analysis of more than 15,000 full-length human

sequences. If α is a sequence, then α^* is the sequence

Golgi network:

CAR LOCATION: Type I membrane protein. Primarily in trans-Golgi.

Cycles between the trans-Golgi network and the cell surface.

DISCUSSION: Also found in strains BAIIB/S, C57BL/6 and DBA/2.

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CC EMBL; DR EMBL; DRR EMBL; AFO041302; BAC30896; BAC36404.1; -.
 CC EMBL; DR EMBL; BCO09143; AHO9143.1; -.
 CC PIR; DR PIR; B56940; B56940.
 MGD; MGI; 105080; fgolnl.
 KW Signal; Transmembrane; Glycoprotein; Repeat; Golgi stack.

SIGNAL	1	17	POTENTIAL	
FT	18	353	TRANS-GOLGI NETWORK INTEGRAL MEMBRAN	
FT	DOMAIN	18	298	PROTEIN 1.
FT	TRANSMEM	299	319	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	320	353	POTENTIAL.
FT	SITE	346	349	CYTOSMERIC (POTENTIAL).
FT	DOMAIN	131	178	ENDOCYTOSIS SIGNAL (BY SIMILARITY).
REPEAT	REPEAT	131	138	6 X 8 AA TANDEM REPEATS.
REPEAT	REPEAT	139	146	1.
REPEAT	REPEAT	147	154	2.
REPEAT	REPEAT	155	162	3.
REPEAT	REPEAT	163	170	4.
REPEAT	REPEAT	171	178	5.
CARBOHYD	110	110	N-LINKED (GLCNAC. . .) (POTENTIAL).	
CARBOHYD	293	293	N-LINKED (GLCNAC. . .) (POTENTIAL).	
SEQUENCE	353 AA:	37848 MW:	95C340C2F4A1EB3 CRC64;	

Query Match Score 12.0%; Score 73; DB 1; Length 353;
 Best Local Similarity 30.5%; Pred. No. 5.1; Mismatches 4; Indels 4;
 Matches 18; Conservative 9; MisMatches 28; IndelS 4;

Qy 32 GTGAAATTGNGNSCLCRDDGGTDSVDTQQQAENSAVPTADTRSPRDPPVRPRR
 Db 148 GDGSKPKTEGSNKATEDDSGKSKTRVLDKPTSKS---PDTERSKTDKVQPTER

RESULT 8

CA13_HUMAN	STANDARD;	PRF;	1466 AA.
ID	CA13_HUMAN		
PO2471	Q15112;		
AC	21-JUL-1986 (Rel. 01, Created)		
DTT	01-JAN-1990 (Rel. 13, Last sequence update)		
DTT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Collagen alpha 1(I) chain precursor.		
GN	CON3A1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NCBI_TAXID	9606 ;		
OX			
RN			
RP	SEQUENCE FROM N.A. TISSUE=Skin fibroblast; MEDLINE=9350838; PubMed=274886;		
RA	Ala-Kokko L., Kontusaari S., Baldwin C.T., Kuijaniemi H., Procock D.J.; "Structure of cDNA clones coding for the entire prepro alpha 1 (I) chain of human type III procollagen. Differences in protein structure from type I procollagen and conservation of codon preferences.", Biochem. J. 260:509-516 (1989)."		
RA	[2]		
RA	SEQUENCE OF 149-1225 FROM N.A. MEDLINE=93B5015; PubMed=2780304;		
RA	Janecko R.A., Ramirez F.; "Nucleotide and amino acid sequences of the entire human alpha 1 (III) collagen," Nucleic Acids Res. 17:6742-6742 (1989)."		
RL	[3]		
RN	SEQUENCE OF 168-398. MEDLINE=7714724; PubMed=557335;		
RX	Seyer J.M., Kang A.H.; "Covalent structure of collagen: amino acid sequence of cyanoac		

les from the amino-terminal segment of type III collagen
.:";
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1 collagen genes during fibroblast growth.";
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Res. 16:7201-7201(1988).
les from the amino-terminal segment of type III collagen
.:";
.: 6.1158-1164(1977).
;1977) to the PIR data bank.
- RP REVIEW ON VARIANTS.
RX MEDLINE=97555959; PubMed=9101290;
RA Kuijvaniemi H., Tramp G., Prockop D.J.;
RT "Mutations in fibrillar collagens (types I, II, III, and XI), fib
associated collagen (type IX), and network-forming collagen (type
cause a spectrum of diseases of bone, cartilage, and blood vessel
RL Hum. Mutat. 9:300-315(1997).
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of the triple helical region of type III collagen in a
Ehlers-Danlos syndrome type IV.";
i. 28:458-463(1991).
IV GLU-1173;
2543; PubMed=1357232;
Richards A.J., Pope F.M., Hopkinson D.A.;
arity 12.0%; Score 73; DB 1; Length 1466;
conservative 10; Mismatches 36; Indels 28; Gaps 7;
LITTLEH---IAHFLGTGGATIMGS-----CICRDNSGT---DDS 55
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
LLALLHPTTILAQQAEEAVGCGSHLQGSYADRQWVKEPCQICVCC- -DGSVNLCDDI 65
QQQQQAENSAVP---TADTRSQRDPVRPRGRGPHEPPR 94
|:|:|:|:|:|:|:|:|:
QELDCPNEIPFGECCAVCPQPETAPTRPP-NGQGPQGPK 108

RE1. 34; Created)
(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
face antigen 2 precursor (MSA-2) (Allelic Form 1).
1 N.A.; PubMed=2090943;
Carr D.A., Carter J.M., Lyon J.A.;
parison of allelic forms of the Plasmodium falciparum
face antigen MSA-2.";
Parasitol. 43:211-220(1990).
May play a role in the merozoite attachment to the
te.
AR LOCATION: Attached to the membrane by a GPI-anchor
[1].
INTL STAGE: During the trophozoite and schizont stages.
ROT entry is copyright. It is produced through a collaboration
Swiss Institute of Bioinformatics and the EMBL outstation -
Bioinformatics Institute. There are no restrictions on its
profit institutions as long as its content is in no way
this statement is not removed. Usage by and for commercial
lires a license agreement. (See http://www.isb-sib.ch/announce/
mail to license@isb-sib.ch).
AAA29697.1; --.
{001136; MSA_2.
}; MSA_2; 1.
brane; Glycoprotein; Antigen; Signal; Repeat;
merozoite.

FT SIGNAL 1 20
FT CHAIN 21 238
FT PROPEP 239 262
FT DOMAIN 44 188
FT DOMAIN 91 98
FT CARBOYD 22 22
FT CARBOYD 36 36
FT CARBOYD 139 139
FT CARBOYD 211 211
FT CARBOYD 235 235
FT CARBOYD 236 236
SQ SEQUENCE 262 AA; 27374 MW; 72E0B2A315E9D154 CRC64;
Query Match 11.9%; Score 72.5%; Pred. No. 4.1;
Best Local Similarity 37.5%; Matches 24; Conservative 6; Mismatches 21; Indels 13;

QY 39 TMGNNSCLCRDSDGTDDSV-----DT----QQQQAENSAVPADTRSQPRDPVR
Db 13.7 TQNNSN--QQSQTNSNVPQDADTKSPTAQPEQENSA-PTAECTESPBLQSA
RESULT 10
MSA2_PLAF7
ID MSA2_PLAF7 STANDARD
AC P50495;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Merozoite surface antigen 2 precursor (MSA-2) (45 kDa merozoite
surface antigen).
GN MSA2.
OS Plasmodium falciparum (isolate 3D7),
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=90205972; PubMed=2181307;
RA Smythe J.A., Peterson M.G., Coppel R.L., Saul A.J., Kemp D.J.,
RA Anders R.P.;
RT "Structural diversity in the 45-kilodalton merozoite surface antigen of Plasmodium falciparum.";
RL Mol. Biochem. Parasitol. 39:227-234(1990).
CC -!- FUNCTION: May play a role in the merozoite attachment to the
CC erythrocyte.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
(CC (potential).
CC -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
Bioinformatics Institute. There are no restrictions on its
CC profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for
CC entities requires a license agreement. (See http://www.isb-sib.ch/)
CC or send an email to license@isb-sib.ch).
CC EMBL: M28891; AAA29686.1;
DR InterPro; IPR01136; MSA_2.
DR Pfam; PF00985; MSA_2; 1.
KW Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
KW GPI-anchor; Merozoite.
FT SIGNAL 1 20
FT CHATN 21 248
FT PROPEP 249 272
FT DOMAIN 44 198
FT DOMAIN 95 108
POLY-THR.

14:34:40 2004

us-10-066-273-9.rsp

arity 37.5%; Pred. No. 4.8;
nservative 6; Mismatches 21; Indels 13; Gaps 4;
CICRDDSGTDSV-----DT-----QQQAENSAVTA
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
nv-QQDSQTKSNPRTQDADTKSPTAQQEAENSA-PTEQTESPELQNSAP
91

236

STANDARD; ERT; 302 AA.

el. 34, Created
el. 34, Last sequence update
el. 34, Last annotation update
ace antigen 2 precursor (MSA-2).
ciparum (isolate tak 9).
solata; Apicomplexa; Haemosporida; Plasmodium.

N.A.
64; PubMed=1990294;
urk J.T., Khan C.M.A., Robinsson J.V., Walliker D.,
life J.G., McBride J.S.;
d antigenic polymorphism of the 35- to 48-kilodalton
ace antigen (MSA-2) of the malaria parasite Plasmodium
1. 11:863-971(1991).

May play a role in the merozoite attachment to the
e
e LOCATION: Attached to the membrane by a GPI-anchor
).

ITAL STAGE: During the trophozoite and schizont stages.

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bioinformatics Institute. There are no restrictions on its
robit institutions as long as its content is in no way
his statement is not removed. Usage by and for commercial
res a license agreement (See <http://www.isb-sib.ch/announce/>
il to license@isb-sib.ch).

CAA37830.1; -.

39615.

01136; MSA_2.

MSA_2; 1.

:name; Glycoprotein; Antigen; Signal; Repeat;
:protozoite;

: 1 20
1 278
9 302

POTENTIAL.
MEROZOITE SURFACE ANTIGEN 2.
HYDROPHOBIC, REMOVED DURING MATURATION
(BY SIMILARITY).

: 4 228

POLYMORPHIC REGION.

: 1 138
12 N-LINKED (GLCNAC. . .) (POTENTIAL).
36 N-LINKED (GLCNAC. . .) (POTENTIAL).
79 N-LINKED (GLCNAC. . .) (POTENTIAL).
51 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
75 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
76 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
2 AA; 30259 MW; 4E0ATB08227CF66 CRC64;

: 11.9%; Score 72.5; DB 1; Length 302;
arity 37.5%; Pred. No. 4.8;

nservative 6; Mismatches 21; Indels 12; Gaps 4;
CICRDDSGTDSV-----DT-----QQQAENSAVTAQQEPVRPRRG 87
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.
 in search, using sw model
 ril 2, 2004, 10:21:14 ; Search time 39 Seconds
 (without alignments)
 946.555 Million cell updates/sec
 -10-066-273-9
 9 MIVFGHAWFLASRSLGCGIL.....QNVDGLVLDTLAVIRLVDK 117
 OSUM62
 pop 10.0 , Gapext 0.5
 17041 seqs, 315518202 residues
 ts satisfying chosen parameters:
 1017041
 3th: 0
 3th: 2000000000
 inimum Match 0%
 axisting Match 100%
 first 45 summaries
 Q9u001 pla
 Q9u00c pla
 Q9u003 the
 Q27033 the
 040912 kai
 P88903 kai
 Q8ixw0 home
 Q8xxh5 ra
 Q9u304 caer
 Q15805 plas
 Q9u0b5 plas
 Q9u0b6 plas
 Q9u0b4 plas
 Q8it83 plas
 Q9puv0 bai
 Q25862 plas
 Q25789 plas
 Q8qrk4 her
 Q42721 peni
 Q8jaki plas
 Q8fml9 cor
 Q81265 her
 Q9u0c3 plas
 Q9u0b3 plas
 Q9u0b1 plas
 Q62313 mus
 Q8gff2 stre
 Q8tov9 droc
 Q8n6u4 home
 Q9s127 art
 Q9sl27

ALIGNMENTS

RESULT 1			
sp_Luman:			
sp_invertebrate:*			
sp_mammal:*			
sp_mhc:*			
sp_organelle:*			
sp_Phage:*			
sp_Plant:*			
sp_Rodent:*			
sp_virus:*			
sp_Vertebrate:*			
sp_unclassified:*			
sp_rvirus:*			
sp_bacteriav:*			
sp_carbohydrat:*			
Q9_CDX4	PRELIMINARY;	PRT;	576 AA.
ID Q96DX4			
AC Q96DX4;			
DT 01-DEC-2001 (TREMBLref. 19, Created)			
DT 01-DEC-2001 (TREMBLref. 19, Last sequence update)			
DT 01-OCT-2003 (TREMBLref. 25, Last annotation update)			
DE Hypothetical protein KIAA1972.			
GN KIAA1972.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.			
OC			

the number of results predicted by chance to have a score of the result being printed, than or equal to the total number of results predicted by chance to have a score of the result being printed.

卷之三

ID	DB	Length	try	Description
.2	576	4	O96DX4	Q96dx4 homo sapien
.2	576	6	Q95LJ3	Q95p3 macaca fasciata
.1	117	11	Q8BLS8	Q8BLs8 mus musculus
.3	576	11	Q8C039	Q8C039 mus musculus
.3	576	11	Q8BYR6	Q8Byr6 mus musculus
.1	601	16	Q8ZT17	Q8zT17 streptomyces
.0	290	5	Q20394	Q20394 caenorhabditis elegans
.1	356	10	Q9A1R4	Q9atR4 oryza sativa
.1	388	10	Q941M8	Q941m8 oryza sativa
.1	388	10	Q8LN68	Q8LN68 oryza sativa
.1	388	10	Q7Y1X7	Q7Y1x7 oryza sativa
.1	5146	5	Q9VXR3	Q9vxR3 drosophila melanogaster
.0	970	10	Q9AYF2	Q9ayF2 oryza sativa
.0	970	10	Q7KF3	Q7kf3 oryza sativa
.9			Q7W0K7	Q7w0K7 alcaligenes faecalis
.8			Q9Z4A0	Q9z4A0
.8			Q7W0K7	Q7w0K7

arity	99.2% ; Score 604 ; DB 4 ; Length 576 ; conservative 100.0% ; Pred. No. 1.2e-57 ; 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;	RX RA RA RT RT RL DR KW SQ	MEDLINE=22354683 ; PubMed=12466851 ; The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation"; 60,770 full-length cDNAs." ; Nature 420: 563-573 (2002). ; EMBL; AAC043522 ; BAC31566.1 ; - . Hypothetical protein. SEQUENCE 117 AA; 12738 MW; D3FEC471ABD5D3C CRC64;
27	GWAVFLASRSIQLGGLITTLEBIAHFLGTGGAATTMNSCICRDDSGTDDSVDTQQ	DB	1 MIVFGWAVFLASRSIQLGGLITTLEBIAHFLGTGGAATTMNSCICRDDSGTDDSVDTQQ
30	GWAVFLASRSIQLGGLITTLEBIAHFLGTGGAATTMNSCICRDDSGTDDSVDTQQ	Db	1 MIVFGWAVFLASRSIQLGGLITTLEBIAHFLGTGGAATTMNSCICRDDSGTDDSVDTQQ
31	NSAVPTADTRSPQRDPVRPRGRGPHEPRRKQNYDGLVLDTLAVRTLVD 116	QY	1 MIVFGWAVFLASRSIQLGGLITTLEBIAHFLGTGGAATTMNSCICRDDSGTDDSVDTQQ
31	NSAVPTADTRSPQRDPVRPRGRGPHEPRRKQNYDGLVLDTLAVRTLVD 116	Db	1 MIVFGWAVFLASRSIQLGGLITTLEBIAHFLGTGGAATTMNSCICRDDSGTDDSVDTQQ
35	RELMINARY;	PRT;	576 AA.
35	RELMINARY;	PRT;	576 AA.
35	TREMBLrel. 19, Created)	Db	1 MIVFGWAVFLASRSIQLGGLITTLEBIAHFLGTGGAATTMNSCICRDDSGTDDSVDTQQ
35	TREMBLrel. 19, Last sequence update)	QY	61 QQAEANSVPTADTRSOPRDPVRPRGRGPHEPRRKQNYDGLVLDTLAVRTLVD
35	TREMBLrel. 25, Last annotation update)	Db	61 QQAEANSVPTADTRSOPRDPVRPRGRGPHEPRRKQNYDGLVLDTLAVRTLVD
DE	protein.		
DE	ularis (Crab eating macaque) (Cynomolgus monkey).		
DE	tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
DE	heria; Primates; Catarrhini; Cercopithecidae;		
DE	ae; Macaca.		
41;			
41;	N.A.		
41;	Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,		
41;	ano S.;		
41;	novel full-length cDNA clones from macaque testis cDNA		
41;	T-2001) to the EMBL/GenBank/DBJ databases.		
41;	5; BA869714.1; - .		
41;	008938; ARM.		
41;	003877; SPRY receptor.		
41;	001841; Znf_Fing.		
41;	1; SPRY; 1.		
41;	4; RING; 1.		
41;	9; SPRY; 1.		
41;	089; ZF_RING_2; 1.		
41;	protein.		
41;	6 AA; 64259 MW;		
41;	68D230AD1C4F5F8D CRC64;		
41;	arity		
41;	96.2% ; Score 586 ; DB 6 ; Length 576 ;		
41;	conservative 97.4% ; Pred. No. 1.1e-55 ;		
41;	0 ; Mismatches 3 ; Indels 0 ; Gaps 0 ;		
41;	RELMINARY;	PRT;	117 AA.
41;	TREMBLrel. 23, Created)	Db	1 MIVFGWAVFLASRSIQLGGLITTLEBIAHFLGTGGAATTMNSCICRDDSGTDDSVDTQQ
41;	TREMBLrel. 23, Last sequence update)	QY	61 QQAEANSVPTADTRSOPRDPVRPRGRGPHEPRRKQNYDGLVLDTLAVRTLVD
41;	TREMBLrel. 23, Last annotation update)	Db	61 QQAEANSVPTADTRSOPRDPVRPRGRGPHEPRRKQNYDGLVLDTLAVRTLVD
41;	(Mouse);		
41;	tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
41;	heria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
41;	090;		
41;	N.A.		
41;	6J; TISSUE=Cortex;		
43;	RELMINARY;	PRT;	117 AA.
43;	TREMBLrel. 23, Created)	Db	1 MIVFGWAVFLASRSIQLGGLITTLEBIAHFLGTGGAATTMNSCICRDDSGTDDSVDTQQ
43;	TREMBLrel. 23, Last sequence update)	QY	61 QQAEANSVPTADTRSOPRDPVRPRGRGPHEPRRKQNYDGLVLDTLAVRTLVD
43;	TREMBLrel. 23, Last annotation update)	Db	61 QQAEANSVPTADTRSOPRDPVRPRGRGPHEPRRKQNYDGLVLDTLAVRTLVD
43;	(Mouse);		
43;	tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
43;	heria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
43;	090;		
43;	N.A.		
43;	6J; TISSUE=Cortex;		
45;	RELMINARY;	PRT;	117 AA.
45;	TREMBLrel. 23, Created)	Db	1 MIVFGWAVFLASRSIQLGGLITTLEBIAHFLGTGGAATTMNSCICRDDSGTDDSVDTQQ
45;	TREMBLrel. 23, Last sequence update)	QY	61 QQAEANSVPTADTRSOPRDPVRPRGRGPHEPRRKQNYDGLVLDTLAVRTLVD
45;	TREMBLrel. 23, Last annotation update)	Db	61 QQAEANSVPTADTRSOPRDPVRPRGRGPHEPRRKQNYDGLVLDTLAVRTLVD
45;	(Mouse);		
45;	tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
45;	heria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
45;	090;		
45;	N.A.		
45;	6J; TISSUE=Cortex;		

;C-1995) to the EMBL/GenBank/DBJ databases.

[N.A.; PubMed=985116;

;cence of the nematode *C.elegans*: A platform for ;biology.";

;012-2018(1998); CAA92502.1; -.

T22161;

012.6; CE03330. MW;

B60BEFE9C89E7780 CRC64;

0 AA;

32831 MW;

B60BEFE9C89E7780 CRC64;

14.0%; Score 85.5; DB 5; Length 290;

;conservative 15; Mismatches 31; Indels 17; Gaps 5;

(Rice).

;ridiplantae; Streptophyta; Embryophyta; Tracheophyta;

; Magnoliophyta; Liliopsida; Poales; Poaceae;

; Oryzeae; Oryza.

;30;

4 N.A.; PubMed=11264415;

;ebley J.;

;olution of the teosinte branched gene among maize and

;yes.";

;rol. 18:627-638 (2001).

;3; AAK37505.1; -.

;24; -.

;2005333; TCP.

;1; TCP; 1.

;FQ;

;56; 356 MW;

95D7174BC6AB8F84 CRC64;

;6 AA;

37757 MW;

95D9GDDOSVDTQQOQAENSA-----VPPADTRSQPDRDPVRPRGRGPHEP

93

;93;

;13.1%; Score 79.5; DB 10; Length 356;

;conservative 6; Mismatches 27; Indels 9; Gaps 1;

;32.3%; Pred. No. 2.4;

;241;

;JEEDGSSSLSVDGKQQHSNPADRGGGAGDHKGRAAHGHSDGKKPAKPRRAAANPKPP

239

;95

;PRELIMINARY;

; PRT; 388 AA.

(TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE Teosinte branched protein.

GN TB1.

OS *Oryza sativa* (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt-

; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

CC Ehrhartoideae; Oryzeae; Oryza.

CX NCBI_TaxID=4540;

RN [1]

RN SEQUENCE FROM N.A.

RC STRAIN=cv. indica guanglu'ai 4;

RP

RT SEQUENCE FROM N.A.

RC STRAIN=cv. indica guanglu'ai 4;

RN

RN SEQUENCE FROM N.A.

RC STRAIN=cv. indica guanglu'ai 4;

RN

RN SEQUENCE FROM N.A.

RC STRAIN=cv. indica guanglu'ai 4;

RN

RN SEQUENCE FROM N.A.

RC STRAIN=cv. indica guanglu'ai 4;

RN

RN SEQUENCE FROM N.A.

RC STRAIN=cv. indica guanglu'ai 4;

RN

RN SEQUENCE FROM N.A.

RC STRAIN=cv. indica guanglu'ai 4;

RN

RN SEQUENCE FROM N.A.

RC STRAIN=cv. indica guanglu'ai 4;

RN

RN SEQUENCE FROM N.A.

RC STRAIN=cv. indica guanglu'ai 4;

RN

RN SEQUENCE FROM N.A.

RC STRAIN=cv. indica guanglu'ai 4;

RN

RN SEQUENCE FROM N.A.

RC STRAIN=cv. indica guanglu'ai 4;

RN

RN SEQUENCE FROM N.A.

RC STRAIN=cv. indica guanglu'ai 4;

RN

RN SEQUENCE FROM N.A.

RC STRAIN=cv. indica guanglu'ai 4;

RN

RN SEQUENCE FROM N.A.

RC STRAIN=cv. indica guanglu'ai 4;

RN

RN SEQUENCE FROM N.A.

RC STRAIN=cv. indica guanglu'ai 4;

RN

RN SEQUENCE FROM N.A.

RC STRAIN=cv. indica guanglu'ai 4;

RN

RN SEQUENCE FROM N.A.

RC STRAIN=cv. indica guanglu'ai 4;

RN

RN SEQUENCE FROM N.A.

RC STRAIN=cv. indica guanglu'ai 4;

RN

RN SEQUENCE FROM N.A.

RC STRAIN=cv. indica guanglu'ai 4;

RN

RN SEQUENCE FROM N.A.

(TREMBLrel. 19, Created)

14:34:40 2004

us-10-066-273-9.rsp

L-trophus (*Ralstonia eutropha*).
Plasmid pRGI.
Leobacteri; *Beta**proteobacteria*; *Burkholderiales*;
Ralstonia.
C.

--

ID NOS: 33142

udomomas aeruginosaa
267

larity 13.0%; Score 79; DB 4; Length 287;
 Conservative 7; Mismatches 24; Indels 4; Gaps 1;

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DSVDRQQQAENSAVPTADTRSOPRDPVRPP-----RRGRGPHEPRRKVNVDG 102
PGKRTQRRDHPGAVARAPGPARPARRPGGLAGRGAGKRRRPRQVPG 70
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Application US/09418710

182

SION: Michael H.
 ION: TRANSCRIPTIONAL REGULATOR
 : 06501-042001
 ATION NUMBER: US/09/418,710
 DATE: 1999-10-15
 ION NUMBER: PCT/JP98/01783
 DATE: 1998-04-17
 ION NUMBER: JP 9/310027
 DATE: 1997-10-24
 ION NUMBER: JP 9/116570
 DATE: 1997-04-18
 ID NOS: 73
 :SEQ for Windows Version 4.0

) sapiens

larity 12.8%; Score 78; DB 4; Length 1527;
 Conservative 12; Mismatches 26; Indels 20; Gaps 3;

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ITDDSVDTQQQAENSAVPTADTRSOPRDPVRPP-----RRGRGPHEPRPR 95
ISDREEEEEEEREEEEEEDYEAVGRLRPRKTIRGKHSTVTPPAARSGRRKPKHSTR 1314
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-----ONVDGLVLDT 107
 QAPPYVDAEVDELVLT 1334
 Application US/09418710

182

SION: Michael H.
 ION: TRANSCRIPTIONAL REGULATOR
 : 06501-042001
 ATION NUMBER: US/09/418,710
 DATE: 1999-10-15
 ION NUMBER: PCT/JP98/01783
 DATE: 1997-10-24
 ION NUMBER: JP 9/116570
 DATE: 1997-04-18
 ID NOS: 73
 :SEQ for Windows Version 4.0

; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-418-710-29

Query Match 12.8%; Score 78; DB 4; Length 1531;
 Best Local Similarity 27.5%; Pred. No. 3.5;
 Matches 22; Conservative 12; Mismatches 26; Indels 20;
 Qy 48 DDSGTDSVDTQQQAENSAVPTADTRSOPRDPVRPP-----RRGRGPHEPRPR 95
 Db 1259 EDDESEEEEEEEREEEEEEDYEAVGRLRPRKTIRGKHSTVTPPAARSGRRKPKHSTR 1314
 Qy 96 KK-----ONVDGLVLDT 107
 Db 1319 QAPKAPPVDDAYDELVLT 1334

RESULT 5
 US-08-466-120-2
 ; Sequence 2, Application US/09466120
 ; Patent No. 5869284
 ; GENERAL INFORMATION:
 ; APPLICANT: CAO, ET AL.
 ; TITLE OF INVENTION: Retinoic Acid Receptor Epsilon
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
 ; ADDRESS: CECCHI, STEWART & OLSTEIN
 ; STREET: 6 BECKER FARM ROAD
 ; CITY: ROSELAND
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 INCH DISKETTE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WORD PERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/466,120
 ; FILING DATE: June 6, 1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/07266
 ; FILING DATE: 24 JUN 94
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: PERRARO, GREGORY D.
 ; REGISTRATION NUMBER: 36,134
 ; REFERENCE/DOCKET NUMBER: 325800-354
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 433 AMINO ACIDS
 ; TYPE: AMINO ACID
 ; STRANDEDNESS:
 ; TOPOLOGY: LINEAR
 ; MOLECULE TYPE: PROTEIN

US-08-466-120-2
 Query Match 12.3%; Score 75; DB 2; Length 433;
 Best Local Similarity 35.0%; Pred. No. 1.5;
 Matches 21; Conservative 12; Mismatches 23; Indels 4;
 Qy 35 GAATGNSCICRDGSDDSVDTQQQAENSAVPTA-DTRSQ-PRDP--VRPPRI
 Db 29 GSQAQGSSCLREARMPSAGGTAGVLEAAFTAILTRAEPSEPBIRPPK

RESULT 6
 PCT-US94-07266-2
 ; Sequence 2, Application PC/TUS9407266

ITION: AL.
ENTION: Retinoic Acid Receptor Epsilon
JENCES: 2
ADDRESS: CARELLA, BYRNE, BAIN, GILFILLAN,
CECHKI, STEWART & OLSTEIN
BECKER FARM ROAD
AND
JERSEY
3A

ABLE FORM:

IBM PS/2 INCH DISKETTE

STEM: MS-DOS

WORD PERFECT 5.1

ATION DATA:

NUMBER: PCT/US94/07266

Concurrently

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INFORMATION:

Docket Number: 325800-125

ITION INFORMATION:

201-994-1700

)1-994-1744

SEQ ID NO: 2:

ACTERISTICS:

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LINEAR

: PROTEIN

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Matches 24; Conservative 24; Indels 26; G

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US-08-865-597A-2

Sequence 2, Application US/08865597A

Patent No. 5973131

GENERAL INFORMATION:

APPLICANT: Cao, Liang

TITLE OF INVENTION: PENNICILLIJUM MARNEFFEI ANTIGENIC PROTEIN 1

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: USA

ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk.

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Chan, Albert Wai Kit

REGISTRATION NUMBER: 36,479

REFERENCE DOCKET NUMBER: 50288-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 462 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-865-597A-2

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US-08-149-097D-35

Sequence 35, Application US/08149097D

Patent No. 5874236

GENERAL INFORMATION:

APPLICANT: Harpold, Michael

sapiens

for Windows Version 4.0

illis, Steven
 Williams, Mark
 edman, Daniel
 McClue, Ann
 brener, Robert HUMAN CALCIUM CHANNEL COMPOSITIONS AND
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 QUENCES: 40
 SE ADDRESS:
 160 Union Street, Haller & McClain
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 ; Patent No. 6171827
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 ; TITLE OF INVENTION: NOVEL PROCOLLAGENS
 ; FILE REFERENCE: d087057PUS LISTING
 ; CURRENT APPLICATION NUMBER: US/09/029,348
 ; CURRENT FILING DATE: 1998-05-07
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ON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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ON: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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DATE: 1999-02-18
NUMBER: US 60/074,788
DATE: 1998-02-18
ON NUMBER: US 60/094,190
DATE: 1998-07-27
NOS: 33142

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; TO THE INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
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1.0	117	12	US-10-081-056-6	Sequence 6, Appli
1.0	117	13	US-10-066-500-9	Sequence 9, Appli
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1.0	117	14	US-10-066-269-9	Sequence 6, Appli
1.0	117	14	US-10-006-85A-6	Sequence 6, Appli
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ALIGNMENTS

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		APPLICANT: Baker, Kevin P.
		APPLICANT: Botstein, David
		APPLICANT: Desnoyers, Luc
		APPLICANT: Baton, Dan L.
		APPLICANT: Ferrara, Napoleone
		APPLICANT: Fong, Sherman
		APPLICANT: Gao, Wei-Qiang
		APPLICANT: Godowski, Paul J.
		APPLICANT: Goddard, Audrey
		APPLICANT: Gurney, Austin L.
		APPLICANT: Hillan, Kenneth J.
		APPLICANT: Pan, James
		APPLICANT: Paoni, Nicholas F.
		APPLICANT: Roy, Margaret Ann
		APPLICANT: Stewart, Victoria A.
		APPLICANT: Tumas, Daniel
		APPLICANT: Watanabe, Colin K.
		APPLICANT: Williams, P. Mickey
		APPLICANT: Wood, William I.
		TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nuc.
		TITLE OF INVENTION: Acids Encoding the Same
		FILE REFERENCE: P28330PC1
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Patent US10081056
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ON, Kevin P.
Ora, Napoleon
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Oltsen, Mary E.
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Olvers, Scott A.
James

On, Nicholas F.
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Ounabale, Colin K.
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 US-10-002-795-9
 Sequence 9, Application US/10002796
 GENERAL INFORMATION:
 Publication No. US2003003205741
 APPLICANT: Avi J. Ashkenazi
 APPLICANT: Kevin P. Baker
 APPLICANT: David A. Borstein
 APPLICANT: Luc Desnoyers
 APPLICANT: Dan L. Eaton
 APPLICANT: Napoleon Ferrara
 APPLICANT: Sherman Fong
 APPLICANT: Wei-Qiang Gao
 APPLICANT: Hanspeier Gerber
 APPLICANT: Mary E. Gerritsen
 APPLICANT: Audrey Goddard
 APPLICANT: Paul J. Godowski
 APPLICANT: Austin L. Gurney
 APPLICANT: Ivar J. Kljavin
 APPLICANT: Jennie P. Mather
 APPLICANT: Mary A. Napier
 APPLICANT: James Pan
 APPLICANT: Nicholas F. Paonni
 APPLICANT: Margaret Ann Roy
 APPLICANT: Timothy A. Stewart
 APPLICANT: Daniel Tumas
 APPLICANT: Colin K. Watanabe
 APPLICANT: P. Mickey Williams
 APPLICANT: William I. Wood
 APPLICANT: Zemin Zang

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
 CURRENT APPLICATION NUMBER: US/10/002-796
 FILE REFERENCE: P3130RCI
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ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLIC
ACIDS ENCODING THE SAME
P31:0R1C2

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 ; GENERAL INFORMATION:
 ; APPLICANT: Avi J. Ashkenazi
 ; APPLICANT: Kevin P. Baker
 ; APPLICANT: David A. Botstein
 ; APPLICANT: Luc Desnoyers
 ; APPLICANT: Dan L. Eaton
 ; APPLICANT: Napoleone Ferrara
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 ; APPLICANT: Wei-Qiang Gao
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 ; APPLICANT: Zemin Zang
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NU
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 ; CURRENT FILING DATE: 2002-02-01
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Sequence 9, Application US/10066269
Publication No. US20030040014A1

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GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Bottstein
APPLICANT: Luc Denoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleon Ferrara
APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeier Gerber
APPLICANT: Mary E. Gerzitsen
APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Klijavin
APPLICANT: Jennie P. Mather
APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni.

RIN
JES
ication US/10006856A
US20030044841A1
ION:
r, Kevin P
stein, David

Cigaret Ann Roy
 Anthony A. Stewart
 Michael Tumanski
 Lin K. Watanabe
 Mickey Williams
 William I. Wood
 Qin Zang

INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

P130R1C8
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IN NUMBER: PCT/US99/21090

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IN NUMBER: PCT/US99/21547

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APPLICANT: Colin K. Watanabe
 APPLICANT: P Mickey Williams
 APPLICANT: William L. Wood
 APPLICANT: Zenin Zang
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 FILE REFERENCE: P130R1C3
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location US/10066193

JS2013004902A1

ON:

J. Ashkenazi

L. Baker

D. A. Borstein

Desnoyers

L. Baton

Leone Ferrara

Man Fong

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Peter Gerber

E. Gerritsen

Rey Goddard

J. Godowski

Lin Gurney

J. Kjavin

Lie P. Mather

A. Napier

S. Pan

Jolas F. Paoni

Jaret Ann Roy

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Tel Tumas

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Query Match 100.0% Score 609; DB 14; Length 117;
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 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nuc
 ACIDS Encoding the Same
 FILE REFERENCE: P2830B1C4

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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Codowski, Paul J.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
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US-10-015-869A-6

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Sequence 6, Application US/10012121A
Publication No. US20030073810A1

TION:
 er, Kevin P.
 tstein, David
 inoyers, Luc
 ion, Dan L.
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 illan, Kenneth J.
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 TION: Secreted and Transmembrane Polypeptides and Nucleic
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○ sapiens
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C_feature
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larity 100.0%; Score 609; DB 14; Length 117;
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 TION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same
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Job time : 41 secs